

 (TM)

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Search: protein - protein database search, using Smith-Waterman algorithm
 Run on: Sat May 13 08:59:53 2000; Maspar time 4.30 Seconds
 302,703 Million cell updates/sec
 Tabular output not generated.

Title: >US-09-331-631-24
 Description: (31-85) from US09331631.pep
 Perfect Score: 425
 Sequence: 1 DEDDRGGSHLQCCVQRCRQ.....DDQOQHGHEDEEQRGRG 55

Scoring table: PAM 150
 Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq35
 1:geneseqp

Statistics: Mean 23.878; Variance 101.499; scale 0.235

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description	Pred. No.
1	425	100.0	637	1	W62837	2.03e-31
2	174	40.9	593	1	W62835	1.55e-07
3	131	30.8	590	1	W62832	1.08e-03
4	129	30.4	666	1	W62828	1.61e-03
5	129	30.4	666	1	W62829	1.61e-03
6	105	24.7	625	1	W62830	1.83e-01
7	105	24.7	898	1	W31853	1.83e-01
8	95	22.4	409	1	W90342	1.24e+00
9	95	22.4	489	1	W90341	1.24e+00
10	89	20.9	525	1	W62831	3.82e+00
11	89	20.9	566	1	R20181	3.82e+00
12	85	20.0	450	1	W46606	8.02e+00
13	84	19.8	97	1	W59348	9.64e+00
14	84	19.8	444	1	W90340	9.64e+00
15	84	19.8	524	1	W90339	9.64e+00
16	84	19.8	624	1	R08222	9.64e+00
17	84	19.8	782	1	W19764	9.64e+00
18	84	19.8	1255	1	W02146	9.64e+00
19	84	19.8	1255	1	W01111	9.64e+00
20	83	19.5	626	1	W22150	1.16e+01
21	83	19.5	1829	1	Y07242	1.16e+01
22	82	19.3	539	1	W33628	1.39e+01
23	80	18.8	374	1	W97834	2.00e+01

ID	Score	Query Match	Length DB	ID	Description	Pred. No.
24	77	18.1	614	1	W22149	3.43e+01
25	77	18.1	614	1	W62834	3.43e+01
26	77	18.1	1382	1	W31867	3.43e+01
27	77	18.1	1433	1	R39568	3.43e+01
28	76	17.9	150	1	P70058	4.10e+01
29	76	17.9	405	1	W33737	4.10e+01
30	76	17.9	451	1	R27721	4.10e+01
31	76	17.9	509	1	R38210	4.10e+01
32	76	17.9	529	1	R38209	4.10e+01
33	76	17.9	554	1	R05271	4.10e+01
34	75	17.6	288	1	W41574	4.90e+01
35	74	17.4	541	1	W37148	5.85e+01
36	74	17.4	709	1	P91934	5.85e+01
37	74	17.4	783	1	W37151	5.85e+01
38	74	17.4	787	1	W37152	5.85e+01
39	74	17.4	802	1	W37153	5.85e+01
40	73	17.2	193	1	W30750	6.98e+01
41	73	17.2	404	1	R27284	6.98e+01
42	73	17.2	712	1	R30749	6.98e+01
43	73	17.2	1529	1	R97985	6.98e+01
44	72	16.9	76	1	R22394	8.32e+01
45	72	16.9	340	1	W81594	8.32e+01

ALIGNMENTS

RESULT 1
 ID W62837 standard; Protein: 637 AA.
 AC W62837.
 DT 27-OCT-1998 (first entry)
 DE Hordeum vulgare antimicrobial protein.
 KW antimicrobial protein; infestation; control.
 OS Hordeum vulgare.
 PN W09827805-A1.
 PD 02-JUL-1998.
 PE 22-DEC-1997; AU0874.
 PR 20-DEC-1996; AU-004275.
 PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
 PI Bower NT, Goulter KC, Green JL, Manners JM, Marcus JP;
 DR WPI: 98-372729/32.
 PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
 useful for controlling microbial infestations of plants or mammals
 PS Claim 1; Page 60-62; 96pp; English.
 CC The sequence is that of an antimicrobial protein which can
 be used to control microbial infestations in plants and mammalian
 CC animals.
 CC Sequence 637 AA.

Query Match 100.0%; Score 425; DB 1; Length 637;
 Best Local Similarity 100.0%; Pred. No. 2.03e-31;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 31 DEDDRGGSHLQCCVQRCRQERPRYSHARCVCRRDQOQHGHEDEEQRGRG 85
 Qy 31 DEDDRGGSHLQCCVQRCRQERPRYSHARCVCRRDQOQHGHEDEEQRGRG 85

RESULT 2
 ID W62835 standard; Protein: 593 AA.
 AC W62835.
 DT 27-OCT-1998 (first entry)
 DE Zea mays antimicrobial protein.
 KW antimicrobial protein; infestation; control.
 OS Zea mays.
 PN W09827805-A1.
 PD 02-JUL-1998.
 PE 22-DEC-1997; AU0874.
 PR 20-DEC-1996; AU-004275.
 PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
 PI Bower NT, Goulter KC, Green JL, Manners JM, Marcus JP;
 DR WPI: 98-372729/32.
 PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
 useful for controlling microbial infestations of plants or mammals

PS Claim 1: Page 58-60; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 593 AA;

Query Match 40.9%; Score 174; DB 1; Length 593;
Best Local Similarity 32.7%; Pred. No. 1.55e-07;
Matches 18; Conservative 22; Mismatches 13; Indels 2; Gaps 2;

DB 27 DNHHHGHSQCVARC-EDRPMHOPRCLQCREREERK-ROERSRHADDRS 79
QY 31 DEDDRRGSHLQOCVORCRQERPRYSNARCVOECRDDQOQHGRHDEEGRG 85

RESULT 3
ID W62832 standard; Protein: 590 AA.

AC W62832:
DT 27-OCT-1998 (first entry)
DE Gossypium hirsutum antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Gossypium hirsutum.
PN W09827805-A1.

PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PT (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.

PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1: Page 49-51; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.

SQ Sequence 590 AA;

Query Match 30.8%; Score 131; DB 1; Length 590;
Best Local Similarity 26.9%; Pred. No. 1.08e-03;
Matches 14; Conservative 23; Mismatches 14; Indels 1; Gaps 1;

DB 114 EEOQOOSORFOECQOHCHQOEPRKQOCVRECRKYOENPMGRERE 165
QY 31 DEDDRRGSHLQOCVORCRQERPRYSNARCVOECRDDQOQHGRHDEEGRG 81

RESULT 4
ID W62828 standard; Protein: 666 AA.

AC W62828:
DT 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.

PT Key Location/Qualifiers
FT Peptide 1..28
FT /note="signal peptide"
FT Protein 29..666
FT /note="mature protein"

PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PT (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB: V42310.

PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1: Page 34-36; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SQ Sequence 666 AA;

Query Match 30.4%; Score 129; DB 1; Length 666;
Best Local Similarity 36.4%; Pred. No. 1.61e-03;
Matches 20; Conservative 14; Mismatches 18; Indels 3; Gaps 2;

DB 182 EEDNKRDPQOEYEDCRRRCQOEPRQOH-OCQLRCRQOHRQGRGDMNPRG 235
QY 31 DEDDRRGSH--SLQOCVORCRQERPRYSNARCVOECRDDQOQHGRHDEEGRG 83

RESULT 5
ID W62829 standard; Protein: 666 AA.

AC W62829:
DT 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.

PT Key Location/Qualifiers
FT Peptide 1..28
FT /note="signal peptide"
FT Protein 29..666
FT /note="mature protein"

PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PT (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.

PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1: Page 39-41; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.

SQ Sequence 666 AA;

Query Match 30.4%; Score 129; DB 1; Length 666;
Best Local Similarity 34.5%; Pred. No. 1.61e-03;
Matches 19; Conservative 16; Mismatches 17; Indels 3; Gaps 2;

DB 182 EEDNKRDPQOEYEDCRRRCQOEPR-QOYQCCRCRQOHRQGRGDLNPRG 235
QY 31 DEDDRRGSH--SLQOCVORCRQERPRYSNARCVOECRDDQOQHGRHDEEGRG 83

RESULT 6
ID W62830 standard; Protein: 625 AA.

AC W62830:
DT 27-OCT-1998 (first entry)
DE Macadamia integrifolia antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Macadamia integrifolia.

PT Key Location/Qualifiers
FT Peptide 1..28
FT /note="signal peptide"
FT Protein 29..666
FT /note="mature protein"

PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997; AU0874.
PR 20-DEC-1996; AU-004275.
PT (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
DR WPI: 98-377279/32.
DR N-PSDB: V42316.

PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PS Claim 1: Page 43-45; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.

SQ Sequence 625 AA; 24.7%; Score 105; DB 1; Length 625;
Query Match Best Local Similarity 31.1%; Pred. No. 1.83e-01;
Matches 14; Conservative 16; Mismatches 12; Indels 3; Gaps 2;
DB 141 EGNKRPDQREYEDCRHRCQDEPRLL-QYOCQRCQDEQRCRGR 184
QY 31 DEDRRRGH--SLQOCVQRCRQERPRYSHARCVOECRDDQOGR 73

RESULT 7
ID W31853 standard; Protein; 898 AA.
AC W31853;
DT 27-APR-1998 (first entry)
KM Mycobacterium tuberculosis 77 kDa protein.
KW Tuberculosis; mycobacteria; infection; diagnosis;
OS Antimycobacterial; antibiotic; vaccine.
PN Mycobacterium tuberculosis.
PI W09741252-A2.
PD 06-NOV-1997.
PF 18-APR-1997; E01973.
PR 29-APR-1996; DE-017184.
PA (GBFR) GBF GES BIOTECH FORSCHUNG GMBH.
PI Espitia C, Honisch C, Moreno C, Singh M;
DR WPI; 97-549750/50.
DR N-PSDB; T93610.
PT New DNA and related proteins or RNA derived from M. tuberculosis -
PT used for diagnosis of mycobacterial infections, monitoring
PT vaccination and development of anti-mycobacterial agents
PS Claim 7; Fig 14, 55pp; English.
CC This novel 77 kDa protein is encoded by an open reading frame of
CC a Mycobacterium tuberculosis DNA fragment (see T93610) containing
CC polymorphic GC-rich sequences. It is highly enriched in glycine
CC and may be a cell wall protein. Novel M. tuberculosis proteins
CC (see W31851-57) are claimed. These can be produced as recombinant
CC proteins, especially in bacterial, yeast, fungal or higher
CC eukaryote host cells, and used for diagnosing tuberculosis and
CC other mycobacterial infections in humans or animals. The claimed
CC proteins can also be used for epidemiological studies, for
CC monitoring vaccination, and for the development of vaccines and
CC anti-mycobacterial drugs.
SQ Sequence 898 AA;

Query Match 24.7%; Score 105; DB 1; Length 898;
Best Local Similarity 31.6%; Pred. No. 1.83e-01;
Matches 12; Conservative 15; Mismatches 10; Indels 1; Gaps 1;
DB 821 CRRVWRRYRRORWCRORRDRORRRORRQSGHAR 858
QY 48 CROERPRYSHAR-CVOECRDDQOGRHNEDEEGRGR 84

RESULT 8
ID W90342 standard; Protein; 409 AA.
AC W90342;
DT 24-MAY-1999 (first entry)
DE G. max truncated SBP2 protein.
KM SBP1: sucrose binding protein; SBP2: sucrose uptake; transgenic plant;
KW seed; carbohydrate content; soybean.
OS Glycine max.
PI W09853086-A1.
PD 26-NOV-1998.
PF 21-MAY-1998; U10465.
PR 22-MAY-1997; US-047568.
PA (UNIV) UNIV WASHINGTON STATE RES FOUND.
PI Chao WS, Grimes HD;
DR WPI; 99-070155/06.
PT New modified plant sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds
PS Claim 7; Page 39-40; 58pp; English.
CC This sequence represents a novel sucrose binding protein, SBP2 isolated

CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
SQ Sequence 489 AA;

Query Match 22.4%; Score 95; DB 1; Length 489;
Best Local Similarity 36.2%; Pred. No. 1.24e+00;
Matches 17; Conservative 11; Mismatches 13; Indels 6; Gaps 5;
DB 39 LVTCKHQCQOQR-QYTESDKRTCLQOC-DSMKOE-REKQVEETREK 82
QY 41 LQOCVQRCRQERPRYSHA--R-CVOECRDDQOGRHNEDEEGRGR 84

RESULT 9
ID W90341 standard; Protein; 489 AA.
AC W90341;
DT 24-MAY-1999 (first entry)
DE G. max SBP2 protein.
KM SBP1: sucrose binding protein; SBP2: sucrose uptake; transgenic plant;
KW seed; carbohydrate content; soybean.
OS Glycine max.
PI W09853086-A1.
PD 26-NOV-1998.
PF 21-MAY-1998; U10465.
PR 22-MAY-1997; US-047568.
PA (UNIV) UNIV WASHINGTON STATE RES FOUND.
PI Chao WS, Grimes HD;
DR WPI; 99-070155/06.
PT New modified plant sucrose binding proteins - used to develop
PT transgenic plants which can have enhanced or decreased sucrose
PT uptake activity in developing seeds
PS Claim 13b; Page 37-38; 58pp; English.
CC This sequence represents a novel sucrose binding protein, SBP2 isolated
CC from Glycine max. This protein is used in a method resulting in the
CC production of a modified plant sucrose binding protein (SBP) which has a
CC modified amino acid sequence compared to a corresponding wild-type SBP,
CC and where expression of the modified SBP in a yeast assay system confers
CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC The products of the invention can be used for producing transgenic plants
CC which have modified sucrose uptake activity, particularly in developing
CC seeds. Enhanced sucrose uptake activity in developing seeds may be
CC desirable where it is an advantage to increase the carbohydrate content
CC of the seed (e.g. where the seed is the primary plant material harvested,
CC such as soybean). In contrast, decreased sucrose uptake activity in
CC seeds might be desirable where the vegetative material of the plant is
CC harvested. The SBP regulatory regions confer specific or enhanced
CC expression in developing seeds and so may be used to express any
CC transgene in developing seeds.
SQ Sequence 489 AA;

Query Match 22.4%; Score 95; DB 1; Length 489;
Best Local Similarity 36.2%; Pred. No. 1.24e+00;
Matches 17; Conservative 11; Mismatches 13; Indels 6; Gaps 5;
DB 39 LVTCKHQCQOQR-QYTESDKRTCLQOC-DSMKOE-REKQVEETREK 82
QY 41 LQOCVQRCRQERPRYSHA--R-CVOECRDDQOGRHNEDEEGRGR 84

RESULT 10

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ID W62831 standard; Protein: 525 AA.
AC W62831;
DE 27-OCT-1998 (first entry)
DE Theobroma cacao antimicrobial protein.
KW antimicrobial protein; infestation; control.
OS Theobroma cacao.
PN W09827805-A1.
PD 02-JUL-1998.
PF 22-DEC-1997: AU0874.
PR 20-DEC-1996: AU-004275.
PA (RENR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
WPI: 98-377279/32.
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PR useful for controlling microbial infestations of plants or mammals
PS Claim 1: Page 47-49; 96pp; English.
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
SC Sequence 525 AA:

Query Match 20.9%; Score 89; DB 1; Length 525;
Best Local Similarity 28.9%; Pred. No. 3.82e+00;
Matches 11; Conservative 14; Mismatches 12; Indels 1; Gaps 1;

DB 86 QOCQGRCEQOQGGREQQOQCKRCKWEQYKEQERGENH 123
OY 42 QOCVORCR-QERPRYSARCVOECRDQOQHGHRHGE 78
II II : : : : : : : : : : : : : : : : : :
II II : : : : : : : : : : : : : : : : : :
DE 16-APR-1992 (first entry)
DE Sequence encoded by 67 kD T. cacao protein cDNA.
KW Cocoa; flavour; vicillin; seed storage protein.
OS Theobroma cacao.
PN W09119801-A.
PD 26-DEC-1991.
PF 07-JUN-1991: G00914.
PR 11-JUN-1990: GB-013016.
PA (MNSC) MARS UK LTD.
PI Spencer ME, Hodge R, Deakin EA, Ashton S;
DR WPI: 92-024418/03.
N-PSDB: Q20377.
PT Recombinant cocoa proteins - are responsible for flavour in cocoa
PT beans and produced in large quantities using yeast and bacterial
PT expression vectors
PS Claim 4: Fig 2; 59pp; English.
CC The inventors claim a 67 kD and 31 kD T. cacao protein, and
CC fragments, and encoding DNAs. The 47 kD and 31 kD proteins are
CC derived from the 67 kD precursor. T. cacao protein cDNA was
CC detected in a cDNA library prepared from immature cocoa beans RNA
CC using a probe based on the AA sequence of a CNR peptide common to
CC the 47 kD and 31 kD polypeptides. Homology searches revealed close
CC homologies between the 67 kD polypeptide and the vicillin, which are
CC seed storage proteins.
SQ Sequence 566 AA:

Query Match 20.9%; Score 89; DB 1; Length 566;
Best Local Similarity 28.9%; Pred. No. 3.82e+00;
Matches 11; Conservative 14; Mismatches 12; Indels 1; Gaps 1;

DB 86 QOCQGRCEQOQGGREQQOQCKRCKWEQYKEQERGENH 123
OY 42 QOCVORCR-QERPRYSARCVOECRDQOQHGHRHGE 78
II II : : : : : : : : : : : : : : : : : :
II II : : : : : : : : : : : : : : : : : :
DE 30-JUN-1998 (first entry)
DE Tyrosine kinase associated protein 1.

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KW tyrosine kinase associated protein-1; TKA-1; antibody;
KW detection; binding agent; diagnosis; treatment;
KW receptor dimerisation.
OS Homo sapiens.
PH Key
FT Protein
FT Location/Qualifiers
FT 7..112
FT /note="domain repeated in 146-252 and 346-376"
FT 146..252
FT /note="repeated from region 7-112"
FT 346..376
FT /note="repeated from region 7-112"
FT 7..89
FT /label="GLGF domain"
FT /label="protein-protein signalling interactions"
FT 145..229
FT /label="GLGF domain"
FT /note="Protein-protein signalling interactions"
FN W09801551-A1.
PD 15-JAN-1998.
PF 16-OCT-1996: U16510.
PR 13-JUN-1996: US-666067.
PR 13-JUN-1996: US-665037.
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
PI Seedorf L, Ullrich A;
DR WPI: 98-101049/09.
PT Tyrosine kinase associated protein-1 - used for the diagnosis and
PT treatment of TKA-1 related diseases
PS Claim 2: Fig 1; 61pp; English.
CC The Tyrosine kinase associated protein-1 (TKA-1) contains a stretch
CC of 106 amino acids (aa/112) which is duplicated within the
CC sequence (aa 146-252) with 65% identity, and again (aa346-176) with
CC 47% identity. A binding agent of TKA-1, able to bind to a TKA-1
CC polypeptide, or the full length TKA-1 protein can both be used in a
CC method for disrupting or promoting receptor dimerisation. They can
CC also be used to identify agents capable of interfering with the
CC interaction between them. The TKA-1 antibody can be used for the
CC detection of TKA-1. The TKA-1 protein, antibody and binding agent can
CC all be used in the diagnosis and treatment of TKA-1 related diseases and
CC conditions.
SQ Sequence 450 AA:

Query Match 20.0%; Score 85; DB 1; Length 450;
Best Local Similarity 33.3%; Pred. No. 8.02e+00;
Matches 13; Conservative 13; Mismatches 10; Indels 3; Gaps 3;

DB 398 QODGRGREN-QCERSESETERERERERERERESERARG 435
OY 49 QOERPRYSARCVOEC-RDQOQHGHRH-EQEEQGRG 85
II II : : : : : : : : : : : : : : : : : :
II II : : : : : : : : : : : : : : : : : :
DE 08-SEP-1998 (first entry)
DE Human ErbB2 extracellular domain protein fragment (aa 529-625).
DE ErbB2; epitope; monoclonal antibody; identification; apoptosis;
KW detection; treatment; disorder; tumour; benign; malignant; leukemia;
KW lymphoid malignancy; inflammation; angiogenic; immunological.
OS Homo sapiens.
PN W09817797-A1.
PD 30-APR-1998.
PF 09-OCT-1997: U18385.
PR 18-OCT-1996: US-731794.
PA (GENTECH) GENENTECH INC.
PA (GENTECH) UNIV TEXAS SYSTEM.
PI Fendly BM, Phillips GD, Scheuermann RH, Uhr JW;
DR WPI: 98-261493/23.
PT New anti-ErbB2 antibodies - which induce apoptosis in cells which
PT overexpress ErbB2, used to treat e.g. tumours or inflammatory,
PT angiogenic or immunologic disorders
PS Disclosure; Page 46; 72pp; English.
CC This sequence represents a fragment of the human ErbB2 extracellular
CC domain corresponding to amino acids 529-625 which is capable of binding

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CC monoclonal antibodies 4D5. This region is used in a method which
 CC identifies antibodies capable of binding to ErbB2 and induce apoptosis of
 CC a cell which overexpresses ErbB2. The antibodies can also be used to
 CC detect ErbB2 on a cell. The antibodies can be used for treating disorders
 CC such as benign or malignant tumours, (e.g. renal, liver, kidney, bladder,
 CC breast, gastric, ovarian, colorectal, prostate, pancreatic, lung, vulval,
 CC thyroid, hepatic carcinomas, sarcomas, glioblastomas, and various head
 CC and neck tumours), leukemias and lymphoid malignancies, other disorders
 CC such as neuronal, glial, astrocytic, hypothalamic and other glandular
 CC macrophage, epithelial, stromal and blastocoele disorders, and
 CC inflammatory, angiogenic and immunologic disorders.
 SQ Sequence 97 AA;

Query Match 19.8%; Score 84; DB 1; Length 97;
 Best Local Similarity 44.4%; Pred. No. 9.64e+00;
 Matches 16; Conservative 7; Mismatches 7; Indels 6; Gaps 5;
 DB 10 QCEVGRVYLGIPREVNARHCLP-CHPCQFONG 44
 QY 42 QOCVGRCR--QERPR-YSHAR-CVQECRD-000HG 72

RESULT 14
 ID W90340 standard; protein: 444 AA.
 AC W90340;
 DT 24-MAY-1999 (first entry)
 DE G. max truncated SBP1 protein.
 KM SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 KW seed; carbohydrate content; soybean.
 OS Glycine max.
 PN W09853086-A1.
 PD 26-NOV-1998.
 PE 21-MAY-1998; U10465.
 PR 22-MAY-1997; US-047568.
 RA (UNITW) UNIV WASHINGTON STATE RES FOUND.
 PI Chao WS, Grimes HD;
 PT WPI; 99-070155/06.
 PT New modified plant sucrose binding proteins - used to develop
 PT transgenic plants which can have enhanced or decreased sucrose
 PT uptake activity in developing seeds
 PS Claim 7, Page 36-37; 58pp; English.
 CC This sequence represents a novel sucrose binding protein, SBP1 isolated
 CC from Glycine max. This protein is used in a method resulting in the
 CC production of a modified plant sucrose binding protein (SBP) which has a
 CC modified amino acid sequence compared to a corresponding wild-type SBP,
 CC and where expression of the modified SBP in a yeast assay system confers
 CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
 CC The products of the invention can be used for producing transgenic plants
 CC which have modified sucrose uptake activity, particularly in developing
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be
 CC desirable where it is an advantage to increase the carbohydrate content
 CC of the seed (e.g. where the seed is the primary plant material harvested,
 CC such as soybean). In contrast, decreased sucrose uptake activity in
 CC seeds might be desirable where the vegetative material of the plant is
 CC harvested. The SBP regulatory regions confer specific or enhanced
 CC expression in developing seeds and so may be used to express any
 CC transgene in developing seeds.
 SQ Sequence 444 AA;

Query Match 19.8%; Score 84; DB 1; Length 444;
 Best Local Similarity 29.2%; Pred. No. 9.64e+00;
 Matches 14; Conservative 14; Mismatches 15; Indels 5; Gaps 4;

DB 40 LVTKKHQCCQQQ-QYTEGDKRVCLSCDRYHNRKQERKQIOETREK 86
 QY 41 LOOCVGRCRQERPRYSHA--R-CVQEC-RDDQOQHGRHDEEFGGR 84

RESULT 15
 ID W90339 standard; protein: 524 AA.
 AC W90339;
 DT 24-MAY-1999 (first entry)
 DE G. max SBP1 protein.

KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 KM seed; carbohydrate content; soybean.
 OS Glycine max.
 PN W09853086-A1.
 PD 26-NOV-1998.
 PE 21-MAY-1998; U10465.
 PR 22-MAY-1997; US-047568.
 RA (UNITW) UNIV WASHINGTON STATE RES FOUND.
 PI Chao WS, Grimes HD;
 PT WPI; 99-070155/06.
 PT New modified plant sucrose binding proteins - used to develop
 PT transgenic plants which can have enhanced or decreased sucrose
 PT uptake activity in developing seeds
 PS Disclosure; Page 34-36; 58pp; English.
 CC This sequence represents a novel sucrose binding protein, SBP1 isolated
 CC from Glycine max. This protein is used in a method resulting in the
 CC production of a modified plant sucrose binding protein (SBP) which has a
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 CC of the seed (e.g. where the seed is the primary plant material harvested,
 CC such as soybean). In contrast, decreased sucrose uptake activity in
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 CC harvested. The SBP regulatory regions confer specific or enhanced
 CC expression in developing seeds and so may be used to express any
 CC transgene in developing seeds.
 SQ Sequence 524 AA;

Query Match 19.8%; Score 84; DB 1; Length 524;
 Best Local Similarity 29.2%; Pred. No. 9.64e+00;
 Matches 14; Conservative 14; Mismatches 15; Indels 5; Gaps 4;

DB 40 LVTKKHQCCQQQ-QYTEGDKRVCLSCDRYHNRKQERKQIOETREK 86
 QY 41 LOOCVGRCRQERPRYSHA--R-CVQEC-RDDQOQHGRHDEEFGGR 84

Search completed: Sat May 13 09:00:01 2000
 Job time : 8 secs.

